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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/932,812

OIPE

DATE: 01/07/2002
TIME: 13:24:28

Input Set: I932812.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Sun, Lee-Hwei K
2 Sun, Bill N
3 Sun, Cecily R
4 <120> TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased
5 <130> FILE REFERENCE: 02SUN2001
6 <140> CURRENT APPLICATION NUMBER: US/09/932,812
7 <141> CURRENT FILING DATE: 2001-10-30
8 <160> NUMBER OF SEQ ID NOS: 22
9 <170> SOFTWARE: PatentIn version 3.1
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37 <213> ORGANISM: Artificial Sequence
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42 <210> SEQ ID NO 5
43 <211> LENGTH: 29
44 <212> TYPE: DNA

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63 <223> OTHER INFORMATION: PCR primer
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66     ttgtgtcga                                         69
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143 <212> TYPE: DNA
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145 <220> FEATURE:
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149      ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac      120
150      agccgagtc tggagaggta cctcttggag gccaaaggagg ccgagaatat cacgacgggc      180
151      tgtgtgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc      240
152      tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc      300
153      ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg      360
154      gagccctgc agctgcatgt ggataaagcc gtcagtggcc ttgcagcct caccactctg      420
155      cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctgagctgct      480
156      ccactccgaa caatcactgc tgacactttc cgaaactct tccgagtcta ctccaatttc      540
157      ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt      600
158      ggcggttccg gtggaggcgg aagcggcggg ggaggatcag agcgcaaagt ttgtgtcgag      660
159      tgcccacgt gccagcacc acctgtggca ggaccgtcag tcttcctctt cccccaaaa      720
160      cccaaggaca cctcatgat ctcccgacc cctgaggtca cgtgcgtggg ggtggacgtg      780
161      agccacgaag accccgaggt ccagttcaac tggtagctgg acggcgtgga ggtgcataat      840
162      gccaaagaca agccacggga ggagcagttc aacagcacgt tccgtgtggg cagcgtcctc      900
163      accgttgtgc accaggactg gctgaacggc aaggagtaca agtgcaaggc ctccaacaaa      960
164      ggcctcccag cctccatcga gaaaaccatc tccaaaacca aagggcagcc ccgagaacca      1020
165      caggtgtaca cctgcccc atcccgggag gagatgacca agaaccaggc cagcctgacc      1080
166      tgctgtgtca aaggcttcta cccagcgac atcgccgtgg agtgggagag caatgggcag      1140
167      ccggagaaca actacaagac cacacctccc atgctggact ccgacggctc cttcttcctc      1200
168      tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc      1260
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176 <223> OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (F
177 A)
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180      1          5          10          15
181      Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
182      20          25          30
183      Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
184      35          40          45
185      Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
186      50          55          60
187      Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
188      65          70          75          80
189      Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
190      85          90          95
191      Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
192      100         105         110
193      Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
194      115         120         125

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195      Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
196          130                      135                      140
197      Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
198      145                      150                      155                      160
199      Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
200                      165                      170                      175
201      Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
202                      180                      185                      190
203      Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
204          195                      200                      205
205      Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
206          210                      215                      220
207      Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
208      225                      230                      235                      240
209      Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
210                      245                      250                      255
211      His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
212          260                      265                      270
213      Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
214          275                      280                      285
215      Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
216          290                      295                      300
217      Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Ser
218      305                      310                      315                      320
219      Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
220          325                      330                      335
221      Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
222          340                      345                      350
223      Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
224          355                      360                      365
225      Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
226          370                      375                      380
227      Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
228      385                      390                      395                      400
229      Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
230          405                      410                      415
231      Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
232          420                      425                      430
233      Ser Pro Gly Lys
234          435
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237      <212> TYPE: DNA
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243      ctgctgtcgc tccctctggg cctcccagtc ctgggcgcc caccacgcct catctgtgac      120
244      agccgagtc tggagaggta cctcttggag gcccaaggagg ccgagaatat cagcaggggc      180

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VERIFICATION SUMMARY
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Line ? Error/Warning

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